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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/638,648

DATE: 08/24/2000
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Input Set : A:\620971.app
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ENTERED

3 <110> APPLICANT: Stern, David M.
 4 Schmidt, Ann Marie
 5 Yan, Shi Du
 6 Zlokovic, Berislav
 8 <120> TITLE OF INVENTION: A METHOD TO INCREASE CEREBRAL BLOOD FLOW IN AMYLOID
 9 ANGIOPATHY
 11 <130> FILE REFERENCE: 0575/62097
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/638,648
 14 <141> CURRENT FILING DATE: 2000-08-14
 16 <160> NUMBER OF SEQ ID NOS: 6
 18 <170> SOFTWARE: PatentIn Ver. 2.1
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 416
 22 <212> TYPE: PRP
 23 <213> ORGANISM: Bos Taurus
 25 <400> SEQUENCE: 1
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 29 Gly Gly Thr Val Thr Gly Asp Gln Asn Ile Thr Ala Arg Ile Gly Lys
 30 20 25 30
 32 Pro Leu Val Leu Asn Cys Lys Gly Ala Pro Lys Lys Pro Pro Gln Gln
 33 35 40 45
 35 Leu Glu Trp Lys Leu Asn Thr Gly Arg Thr Glu Ala Trp Lys Val Leu
 36 50 55 60
 38 Ser Pro Gln Gly Asp Pro Trp Asp Ser Val Ala Arg Val Leu Pro Asn
 39 65 70 75 80
 41 Gly Ser Leu Leu Leu Pro Ala Val Gly Ile Gln Asp Glu Gly Thr Phe
 42 85 90 95
 44 Arg Cys Arg Ala Thr Ser Arg Ser Gly Lys Glu Thr Lys Ser Asn Tyr
 45 100 105 110
 47 Arg Val Arg Val Tyr Gln Ile Pro Gly Lys Pro Glu Ile Val Asp Pro
 48 115 120 125
 50 Ala Ser Glu Leu Met Ala Gly Val Pro Asn Lys Val Gly Thr Cys Val
 51 130 135 140
 53 Ser Glu Gly Gly Tyr Pro Ala Gly Thr Leu Asn Trp Leu Leu Asp Gly
 54 145 150 155 160
 56 Lys Thr Leu Ile Pro Asp Gly Lys Gly Val Ser Val Lys Glu Glu Thr
 57 165 170 175
 59 Lys Arg His Pro Lys Thr Gly Leu Phe Thr Leu His Ser Glu Leu Met
 60 180 185 190
 62 Val Thr Pro Ala Arg Gly Gly Ala Leu His Pro Thr Phe Ser Cys Ser
 63 195 200 205
 65 Phe Thr Pro Gly Leu Pro Arg Arg Ala Leu His Thr Ala Pro Ile
 66 210 215 220
 68 Gln Leu Arg Val Trp Ser Glu His Arg Gly Gly Glu Gly Pro Asn Val
 69 225 230 235 240
 71 Asp Ala Val Pro Leu Lys Glu Val Gln Leu Val Val Glu Pro Glu Gly

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74 Gly Ala Val Ala Pro Gly Gly Thr Val Thr Leu Thr Cys Glu Ala Pro
75          260          265          270
77 Ala Gln Pro Pro Pro Gln Ile His Trp Ile Lys Asp Gly Arg Pro Leu
78          275          280          285
80 Pro Leu Pro Pro Gly Pro Met Leu Leu Leu Pro Glu Val Gly Pro Glu
81          290          295          300
83 Asp Gln Gly Thr Tyr Ser Cys Val Ala Thr His Pro Ser His Gly Pro
84          305          310          315          320
86 Gln Glu Ser Arg Ala Val Ser Val Thr Ile Ile Glu Thr Gly Glu Glu
87          325          330          335
89 Gly Thr Thr Ala Gly Ser Val Glu Gly Pro Gly Leu Glu Thr Leu Ala
90          340          345          350
92 Leu Thr Leu Gly Ile Leu Gly Gly Leu Gly Thr Val Ala Leu Leu Ile
93          355          360          365
95 Gly Val Ile Val Trp His Arg Arg Arg Gln Arg Lys Gly Gln Glu Arg
96          370          375          380
98 Lys Val Pro Glu Asn Gln Glu Glu Glu Glu Glu Arg Ala Glu Leu
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109 <211> LENGTH: 1426
110 <212> TYPE: DNA
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113 <400> SEQUENCE: 2
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115 gggacagtca cgggggacca aaacatcaca gcccgatcg ggaagccact ggtgctgaac 120
116 tgcaagggag cccccaagaa accacccag cagctggaat ggaactgaa cacaggcccg 180
117 acagaagctt gaaagtccct gtctcccccag ggagaccctt gggatagcgt ggctcgggtc 240
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119 tgccggggcaa cgagccggag cggaaaggag accaagtcta actaccgagt ccgagtctat 360
120 cagattcctg ggaagccaga aattgttgat cctgcctctg aactcatggc tgggtgtccc 420
121 aataaggttg ggacatgtgt gtccgagggg ggctaccctg cagggactct taactggctc 480
122 ttggatggga aaactctgat tctctatggc aaaggagtgt cagtgaagga agagaccaag 540
123 agacacccaa agacagggct ttccacgctc cattcggagc tgatggtgac cccagctcgg 600
124 ggaggagctc tccacccac cttctcctgt agcttcaccc ctggccttcc ccggcgccga 660
125 gccctgcaca cggcccccat ccagctcagg gtctggagtg agcaccgagg tggggagggc 720
126 cccaacgtgg acgctgtgcc actgaaggaa gtccagttgg tggtagagcc agaaggggga 780
127 gcagttagctc ctgggtgtac tgtgaccttg acctgtgaag ccccccacca gcccacact 840
128 caaatccact ggatcaagga tggcaggccc ctgccccttc cccctggccc catgctgctc 900
129 ctcccagagg tagggcctga ggaccaggga acctacagtt gtgtggccac ccatcccagc 960
130 catgggcccc aggagagccg tgctgtcagc gtcacgatca tcgaaacagg cgaggagggg 1020
131 acgactgcag gctctgtgga agggccgggg ctggaacccc tagccctgac cctggggatc 1080
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133 caacgcaaa gacaggagag gaaggtcccg gaaaaccagg aggaggaaga ggaggagaga 1200
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135 ggagcccacg gccagaccg atccatcagc cccttttctt tcccacact ctgttctggc 1320
136 cccagaccag ttctctctg tataatctcc agcccacatc tcccaaaact tcttcacaa 1380

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143 <213> ORGANISM: Human
145 <400> SEQUENCE: 3
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149 Trp Gly Ala Val Gly Ala Gln Asn Ile Thr Ala Arg Ile Gly Glu
150 20 25 30
152 Pro Leu Val Leu Lys Cys Lys Gly Ala Pro Lys Lys Pro Pro Gln Arg
153 35 40 45
155 Leu Glu Trp Lys Leu Asn Thr Gly Arg Thr Glu Ala Trp Lys Val Leu
156 50 55 60
158 Ser Pro Gln Gly Gly Gly Pro Trp Asp Ser Val Ala Arg Val Leu Pro
159 65 70 75 80
161 Asn Gly Ser Leu Phe Leu Pro Ala Val Gly Ile Gln Asp Glu Gly Ile
162 85 90 95
164 Phe Arg Cys Arg Ala Met Asn Arg Asn Gly Lys Glu Thr Lys Ser Asn
165 100 105 110
167 Tyr Arg Val Arg Val Tyr Gln Ile Pro Gly Lys Pro Glu Ile Val Asp
168 115 120 125
170 Ser Ala Ser Glu Leu Thr Ala Gly Val Pro Asn Lys Val Gly Thr Cys
171 130 135 140
173 Val Ser Glu Gly Ser Tyr Pro Ala Gly Thr Leu Ser Trp His Leu Asp
174 145 150 155 160
176 Gly Lys Pro Leu Val Pro Asn Glu Lys Gly Val Ser Val Lys Glu Gln
177 165 170 175
179 Thr Arg Arg His Pro Glu Thr Gly Leu Phe Thr Leu Gln Ser Glu Leu
180 180 185 190
182 Met Val Thr Pro Ala Arg Gly Gly Asp Pro Arg Pro Thr Phe Ser Cys
183 195 200 205
185 Ser Phe Ser Pro Gly Leu Pro Arg His Arg Ala Leu Arg Thr Ala Pro
186 210 215 220
188 Ile Gln Pro Arg Val Trp Glu Pro Val Pro Leu Glu Glu Val Gln Leu
189 225 230 235 240
191 Val Val Glu Pro Glu Gly Gly Ala Val Ala Pro Gly Gly Thr Val Thr
192 245 250 255
194 Leu Thr Cys Glu Val Pro Ala Gln Pro Ser Pro Gln Ile His Trp Met
195 260 265 270
197 Lys Asp Gly Val Pro Leu Pro Leu Pro Pro Ser Pro Val Leu Ile Leu
198 275 280 285
200 Pro Glu Ile Gly Pro Gln Asp Gln Gly Thr Tyr Ser Cys Val Ala Thr
201 290 295 300
203 His Ser Ser His Gly Pro Gln Glu Ser Arg Ala Val Ser Ile Ser Ile
204 305 310 315 320
206 Ile Glu Pro Gly Glu Glu Gly Pro Thr Ala Gly Ser Val Gly Gly Ser
207 325 330 335
209 Gly Leu Gly Thr Leu Ala Leu Ala Leu Gly Ile Leu Gly Gly Leu Gly

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Output Set: N:\CRF3\08232000\I638648.raw

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210          340          345          350
212 Thr Ala Ala Leu Leu Ile Gly Val Ile Leu Trp Gln Arg Arg Gln Arg
213          355          360          365
215 Arg Gly Glu Glu Arg Lys Ala Pro Glu Asn Gln Glu Glu Glu Glu
216          370          375          380
218 Arg Ala Glu Leu Asn Gln Ser Glu Glu Pro Glu Ala Gly Glu Ser Ser
219 385          390          395          400
221 Thr Gly Gly Pro
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226 <211> LENGTH: 1391
227 <212> TYPE: DNA
228 <213> ORGANISM: Human
230 <400> SEQUENCE: 4
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232 gtagtgctc aaaacatcac agcccggtatt ggcgagccac tgggtgctgaa gtgtaagggg 120
233 gcccccaaga aaccacccca gcggtggaa tggaaactga acacaggccg gacagaagct 180
234 tggaaaggtcc tgtctcccca gggaggaggg cctggggaca gtgtggctcg tgtccttccc 240
235 aacggctccc tcttcttccc ggctgtcggg atccaggatg aggggatttt ccggtgcagg 300
236 gcaatgaaca ggaatggaaa ggagaccaag tccaactacc ggtccgtgt ctaccagatt 360
237 cctgggaagc cagaaattgt agattctgcc tctgaactca cggtgtgtgt tcccaataag 420
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239 gggaaagccc tgggtgcctaa tgagaagggg gtatctgtga aggaacagac caggagacac 540
240 cctgagacag ggctcttcac actgcagtcg gagctaattg tgacccagc ccggggagga 600
241 gatccccgtc ccaccttctc ctgtagcttc agcccaggcc tccccgaca ccgggccttg 660
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244 gtccctgccc agccctctcc tcaaatccac tggatgaagg atggtgtgcc cttgccctt 840
245 cccccagccc ctgtgtgat cctccctgag atagggcctc aggaccaggg aacctacagc 900
246 tgtgtggcca cccattccag ccacgggccc caggaaagcc gtgctgtcag catcagcatc 960
247 atcgaaccag gcgaggaggg gccaaactga ggctctgtgg gaggatcagg gctgggaact 1020
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251 actgaggggc cttgaggggc ccacagacag atcccatcca tcagctccct tttcttttcc 1260
252 ccttgaactg ttctggcctc agaccaactc tctctgtat aatctctctc ctgtataacc 1320
253 ccaccttgcc aagctttctt ctacaaccag agccccccac aatgatgatt aaacacctga 1380
254 cacatcttgc a
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258 <211> LENGTH: 403
259 <212> TYPE: PRT
260 <213> ORGANISM: Mouse
262 <400> SEQUENCE: 5
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266 Trp Gly Ala Val Ala Gly Gly Gln Asn Ile Thr Ala Arg Ile Gly Glu
267          20          25          30
269 Pro Leu Val Leu Ser Cys Lys Gly Ala Pro Lys Lys Pro Pro Gln Gln
270          35          40          45
272 Leu Glu Trp Lys Leu Asn Thr Gly Arg Thr Glu Ala Trp Lys Val Leu

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273      50      55      60
275 Ser Pro Gln Gly Gly Pro Trp Asp Ser Val Ala Gln Ile Leu Pro Asn
276 65      70      75      80
278 Gly Ser Leu Leu Leu Pro Ala Thr Gly Ile Val Asp Glu Gly Thr Phe
279      85      90      95
281 Arg Cys Arg Ala Thr Asn Arg Arg Gly Lys Glu Val Lys Ser Asn Tyr
282      100      105      110
284 Arg Val Arg Val Tyr Gln Ile Pro Gly Lys Pro Glu Ile Val Asp Pro
285      115      120      125
287 Ala Ser Glu Leu Thr Ala Ser Val Pro Asn Lys Val Gly Thr Cys Val
288      130      135      140
290 Ser Glu Gly Ser Tyr Pro Ala Gly Thr Leu Ser Trp His Leu Asp Gly
291 145      150      155      160
293 Lys Leu Leu Ile Pro Asp Gly Lys Glu Thr Leu Val Lys Glu Glu Thr
294      165      170      175
296 Arg Arg His Pro Glu Thr Gly Leu Phe Thr Leu Arg Ser Glu Leu Thr
297      180      185      190
299 Val Ile Pro Thr Gln Gly Gly Thr Thr His Pro Thr Phe Ser Cys Ser
300      195      200      205
302 Phe Ser Leu Gly Leu Pro Arg Arg Arg Pro Leu Asn Thr Ala Pro Ile
303      210      215      220
305 Gln Leu Arg Val Arg Glu Pro Gly Pro Pro Glu Gly Ile Gln Leu Leu
306 225      230      235      240
308 Val Glu Pro Glu Gly Gly Ile Val Ala Pro Gly Gly Thr Val Thr Leu
309      245      250      255
311 Thr Cys Ala Ile Ser Ala Gln Pro Pro Pro Gln Val His Trp Ile Lys
312      260      265      270
314 Asp Gly Ala Pro Leu Pro Leu Ala Pro Ser Pro Val Leu Leu Leu Pro
315      275      280      285
317 Glu Val Gly His Ala Asp Glu Gly Thr Tyr Ser Cys Val Ala Thr His
318      290      295      300
320 Pro Ser His Gly Pro Gln Glu Ser Pro Pro Val Ser Ile Arg Val Thr
321 305      310      315      320
323 Glu Thr Gly Asp Glu Gly Pro Ala Glu Gly Ser Val Gly Glu Ser Gly
324      325      330      335
326 Leu Gly Thr Leu Ala Leu Ala Leu Gly Ile Leu Gly Gly Leu Gly Val
327      340      345      350
329 Val Ala Leu Leu Val Gly Ala Ile Leu Trp Arg Lys Arg Gln Pro Arg
330      355      360      365
332 Arg Glu Glu Arg Lys Ala Pro Glu Ser Gln Glu Asp Glu Glu Glu Arg
333      370      375      380
335 Ala Glu Leu Asn Gln Ser Glu Glu Ala Glu Met Pro Glu Asn Gly Ala
336 385      390      395      400
338 Gly Gly Pro
342 <210> SEQ ID NO: 6
343 <211> LENGTH: 1347
344 <212> TYPE: DNA
345 <213> ORGANISM: Mouse
347 <400> SEQUENCE: 6

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VERIFICATION SUMMARY

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